

	Type	L #	Hits	Search Text	Dbs	Time Stamp	Comments	Error Definition	Errors
1	BRS	L1	121	phospholamban	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:43			0
2	BRS	L2	32	phospholamban same (deactivat\$3 or bind\$3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:44			0
3	BRS	L3	67	phospholamban same inhibit\$3	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:45			0
4	BRS	L4	3158	cyclic adj peptide	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:46			0
5	BRS	L5	11900	(molecular adj model\$3) or (computer adj model\$3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:46			0
6	BRS	L6	0	5 same (2 or 3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:47			0
7	BRS	L7	1	4 same (2 or 3)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:47			0
8	BRS	L8	1	(cytosolic adj domain) same phospholamban	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:51			0

	Type	L #	Hits	Search Text	Dbs	Time Stamp	Comments	Error Definition	Error Count
9	BRS	L9	4	caAtPase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:51			0
10	BRS	L10	34	ca-AtPase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:51			0
11	BRS	L11	2	(caAtPase or ca-AtPase) same phospholamban	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/08/11 17:52			0

FILE 'MEDLINE' ENTERED AT 18:02:07 ON 11 AUG 2003

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FILE 'AGRICOLA' ENTERED AT 18:02:07 ON 11 AUG 2003

=> s phospholamban  
L1 5880 PHOSPHOLAMBAN

=> s l1 (p) (inhibit? or deactivat?)  
L2 1548 L1 (P) (INHIBIT? OR DEACTIVAT?)

=> s cyclic peptide  
L3 11269 CYCLIC PEPTIDE

=> s l2 (p) l3  
L4 0 L2 (P) L3

=> s (molecular model?) or (computer model?)  
L5 117423 (MOLECULAR MODEL?) OR (COMPUTER MODEL?)

=> s l2 (p) l5  
L6 15 L2 (P) L5

=> duplicateremove l6  
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove  
DUPLICATE PREFERENCE IS 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH'  
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n  
PROCESSING COMPLETED FOR L6  
L7 5 DUPLICATE REMOVE L6 (10 DUPLICATES REMOVED)

=> d l7 1-15 ibib abs

L7 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2003:78629 CAPLUS  
DOCUMENT NUMBER: 138:250620  
TITLE: Modeling of the inhibitory interaction of  
phospholamban with the Ca<sup>2+</sup> ATPase  
AUTHOR(S): Toyoshima, Chikashi; Asahi, Michio; Sugita, Yuji;  
Khanna, Reena; Tsuda, Takeo; MacLennan, David H.  
CORPORATE SOURCE: Institute of Molecular and Cellular Biosciences,  
University of Tokyo, Tokyo, 113-0032, Japan  
SOURCE: Proceedings of the National Academy of Sciences of the  
United States of America (2003), 100(2), 467-472  
CODEN: PNASA6; ISSN: 0027-8424  
PUBLISHER: National Academy of Sciences  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB The inhibitory interaction of phospholamban (PLN) with the sarco(endo)plasmic reticulum Ca<sup>2+</sup> ATPase isoform 1 (SERCA1a) was modeled on the basis of several constraints which included (i) spontaneous formation of SS-bridges between mutants L321C in transmembrane helix 4 (M4) of SERCA1a and N27C in PLN and between V89C (M4) and V49C (PLN); (ii) definition of the face of the PLN transmembrane helix that interacts with SERCA; (iii) crosslinking between Lys-3 of PLN and Lys-397 and Lys-400 of SERCA2a. The crystal structure of SERCA1a in the absence of Ca<sup>2+</sup>, which binds PLN, was used as the structure into which an at. model of PLN was built. PLN can fit into a transmembrane groove formed by the juxtaposition of M2, the upper part of M4, M6, and M9. In the SERCA1a structure with bound Ca<sup>2+</sup>, this groove is closed, accounting for the ability of Ca<sup>2+</sup> to disrupt PLN-SERCA interactions. Near the cytoplasmic surface of the bilayer, the PLN helix is disrupted to prevent its collision with M4. The model can be extended into the cytoplasmic domain

so that Lys-3 in PLN can be cross-linked with Lys-397 and Lys-400 in SERCA1a with little unwinding of the N-terminal helix of PLN

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 5 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 2001553881 MEDLINE

DOCUMENT NUMBER: 21486400 PubMed ID: 11477077

TITLE: Role of cysteine residues in structural stability and function of a transmembrane helix bundle.

AUTHOR: Karim C B; Paterlini M G; Reddy L G; Hunter G W; Barany G; Thomas D D

CORPORATE SOURCE: Departments of Biochemistry, Molecular Biology, and Biophysics, Medicinal Chemistry, University of Minnesota, Minneapolis, Minnesota 55455, USA... cbk@ddt.biochem.umn.edu

CONTRACT NUMBER: 1K02 HL04209 (NHLBI)

DA0037 (NIDA)

GM27906 (NIGMS)

GM51628 (NIGMS)

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Oct 19) 276 (42) 38814-9.

Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200112

ENTRY DATE: Entered STN: 20011016

Last Updated on STN: 20030105

Entered Medline: 20011204

AB To study the structural and functional roles of the cysteine residues at positions 36, 41, and 46 in the transmembrane domain of \*\*\*phospholamban\*\*\* (PLB), we have used Fmoc (N-(9-fluorenyl)methoxycarbonyl) solid-phase peptide synthesis to prepare alpha-amino-n-butyric acid (Abu)-PLB, the analogue in which all three cysteine residues are replaced by Abu. Whereas previous studies have shown that replacement of the three Cys residues by Ala (producing Ala-PLB) greatly destabilizes the pentameric structure, we hypothesized that replacement of Cys with Abu, which is isosteric to Cys, might preserve the pentameric stability. Therefore, we compared the oligomeric structure (from SDS-polyacrylamide gel electrophoresis) and function (\*\*\*inhibition\*\*\* of the Ca-ATPase in reconstituted membranes) of Abu-PLB with those of synthetic wild-type PLB and Ala-PLB. \*\*\*Molecular\*\*\* modeling provides structural and energetic insight into the different oligomeric stabilities of these molecules. We conclude that 1) the Cys residues of PLB are not necessary for pentamer formation or \*\*\*inhibitory\*\*\* function; 2) the steric properties of cysteine residues in the PLB transmembrane domain contribute substantially to pentameric stability, whereas the polar or chemical properties of the sulfhydryl group play only a minor role; 3) the functional potency of these PLB variants does not correlate with oligomeric stability; and 4) acetylation of the N-terminal methionine has neither a functional nor a structural effect in full-length PLB.

L7 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:34634 CAPLUS

DOCUMENT NUMBER: 134:218589

TITLE: Reexamination of the role of the leucine/isoleucine zipper residues of phospholamban in inhibition of the Ca2+ pump of cardiac sarcoplasmic reticulum

AUTHOR(S): Cornea, Razvan L.; Autry, Joseph M.; Chen, Zhenhui; Jones, Larry R.

CORPORATE SOURCE: Department of Medicine and the Krannert Institute of Cardiology, Indiana University School of Medicine, Indianapolis, IN, 46202, USA

SOURCE: Journal of Biological Chemistry (2000), 275(52), 41487-41494

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Phospholamban is a small phosphoprotein inhibitor of the Ca2+-pump in cardiac sarcoplasmic reticulum, which shows a distinct oligomeric distribution between monomers and homopentamers that are stabilized through Leu/Ile zipper interactions. A two-faced model of phospholamban inhibition of the Ca2+-pump was proposed, in which the Leu/Ile zipper

residues located on one face of the transmembrane .alpha.-helix regulate the pentamer to monomer equilibrium, whereas residues on the other face of the helix bind to and inhibit the pump. Here we tested this two-faced model of phospholamban action by analyzing the functional effects of a new series of Leu/Ile zipper mutants. Pentameric stabilities of the mutants were quantified at different SDS concns. We show that several phospholamban mutants with hydrophobic amino acid substitutions at the Leu/Ile zipper region retain the ability to form pentamers but at the same time give the same or even stronger (i.e. L37I-PLB) inhibition of the Ca2+-pump than do mutants that are more completely monomeric. Steric constraints prevent the Leu/Ile zipper residues sequestered in the interior of the phospholamban pentamer from binding to the Ca2+-pump, leading to the conclusion that the zipper residues access the pump from the phospholamban monomer, which is the active inhibitory species. A modified model of phospholamban transmembrane domain action is proposed, in which the membrane span of the phospholamban monomer maintains contacts with the Ca2+-pump around most of its circumference, including residues located in the Leu/Ile zipper region.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 2  
 ACCESSION NUMBER: 2000071613 MEDLINE  
 DOCUMENT NUMBER: 20071613 PubMed ID: 10603946  
 TITLE: Direct spectroscopic detection of molecular dynamics and interactions of the calcium pump and phospholamban.  
 AUTHOR: Thomas D D; Reddy L G; Karim C B; Li M; Cornea R; Autry J M; Jones L R; Stamm J  
 CORPORATE SOURCE: Department of Biochemistry, University of Minnesota Medical School, Minneapolis 55455, USA.. ddt@ddt.biochem.umn.edu  
 CONTRACT NUMBER: GM27906 (NIGMS)  
 HLO6308 (NHLBI)  
 HL49428 (NHLBI)  
 SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1998 Sep 16) 853 186-94. Ref: 23  
 Journal code: 7506858. ISSN: 0077-8923.  
 PUB. COUNTRY: United States  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 General Review; (REVIEW)  
 (REVIEW, TUTORIAL)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 ENTRY MONTH: 200001  
 ENTRY DATE: Entered STN: 20000124  
 Last Updated on STN: 20000124  
 Entered Medline: 20000107

AB In order to test \*\*\*molecular\*\*\* \*\*\*models\*\*\* of cardiac calcium transport regulation, we have used spectroscopy to probe the structures, dynamics, and interactions of the Ca pump (Ca-ATPase) and \*\*\*phospholamban\*\*\* (PLB) in cardiac sarcoplasmic reticulum (SR) and in reconstituted membranes. Electron paramagnetic resonance (EPR) and phosphorescence of probes bound to the Ca pump show that the activity of the pump is quite sensitive to its oligomeric interactions. In cardiac SR, PLB aggregates and \*\*\*inhibits\*\*\* the pump, and both effects are reversed by PLB phosphorylation. Previous analyses of PLB's oligomeric state were only in detergent solutions, so we used EPR and fluorescence to determine the oligomeric structure of PLB in its native state in lipid bilayers. Wild-type PLB is primarily oligomeric in the membrane, while the mutant L37A-PLB is monomeric. For both proteins, phosphorylation shifts the dynamic monomer-oligomer equilibrium toward oligomers, and induces a similar structural change, as indicated by tyrosine fluorescence; yet L37A-PLB is more effective than wild-type PLB in \*\*\*inhibiting\*\*\* and aggregating the pump. Fluorescence energy transfer shows that the Ca pump increases the fraction of monomeric PLB, indicating that the pump preferentially binds monomeric PLB. These results support a reciprocal aggregation model for Ca pump regulation, in which the Ca pump is aggregated and \*\*\*inhibited\*\*\* by association with PLB monomers, and phosphorylation of PLB reverses these effects while decreasing the concentration of PLB monomers. To investigate the structure of the PLB pentamer in more detail, we measured the reactivities of cysteine residues in the transmembrane domain of PLB, and recorded EPR spectra of spin labels attached to these sites. These results support an atomic structural model, based on molecular dynamics simulations and mutagenesis studies, in which the PLB pentamer is stabilized by a leucine-isoleucine zipper within the transmembrane domain.

L7 ANSWER 5 OF 5 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER: 95271668 MEDLINE  
 DOCUMENT NUMBER: 95271668 PubMed ID: 7752243  
 TITLE: Structural model of the phospholamban ion channel complex in phospholipid membranes.  
 AUTHOR: Arkin I T; Rothman M; Ludlam C F; Aimoto S; Engelman D M; Rothschild K J; Smith S O  
 CORPORATE SOURCE: Department of Cell Biology, Yale University School of Medicine, New Haven, CT 06510, USA.  
 CONTRACT NUMBER: GM 22778 (NIGMS)  
 GM 46732 (NIGMS)  
 GM 47527 (NIGMS)  
 SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1995 May 12) 248 (4) 824-34. Journal code: 2985088R. ISSN: 0022-2836.  
 PUB. COUNTRY: ENGLAND: United Kingdom  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 ENTRY MONTH: 199506  
 ENTRY DATE: Entered STN: 19950629  
 Last Updated on STN: 19950629  
 Entered Medline: 19950620

AB \*\*\*Phospholamban\*\*\* is a 52 amino acid residue membrane protein involved with the regulation of calcium levels across sarcoplasmic reticulum membranes in cardiac muscle cells. The N-terminal 30 amino acid residues of the protein are largely hydrophilic and include two sites whose phosphorylation is thought to dissociate an \*\*\*inhibitory\*\*\* complex between \*\*\*phospholamban\*\*\* and  $\text{Ca}^{2+}$  ATPase. The C-terminal 22 amino acid residues are largely hydrophobic, anchor the protein in the membrane and are responsible for  $\text{Ca}^{2+}$  selective ion conductance. Specific interactions between the transmembrane domains stabilize a pentameric protein complex. We have obtained circular dichroism (CD), transmission Fourier transform infrared (FTIR) and attenuated total reflection Fourier transform infrared (ATR-FTIR) spectra of the full-length protein and have compared these results to those from a 28 residue peptide that includes the transmembrane domain. Both proteins reconstituted into phospholipid membranes are largely alpha-helical by CD and FTIR. Polarized ATR-FTIR measurements show that both the cytosolic and transmembrane helices are oriented perpendicular to the membrane plane with a tilt of  $28 (+/- 6)$  degrees with respect to the membrane normal. This tilt angle is in close agreement to that calculated from a model for the transmembrane domain of \*\*\*phospholamban\*\*\* suggested by mutagenesis and \*\*\*molecular\*\*\* \*\*\*modeling\*\*\*. Phosphorylation does not significantly change the secondary structure or orientation of the protein. The pentameric complex is modeled as a left-handed coiled-coil of five long helices (40  $(+/- 3)$  residues) that extend across the membrane from the luminal carboxy terminus to the phosphorylation site in the cytoplasm. The helix bundle forms a perpendicular ion pore that may begin at a distance (17 to 29 Å) from the membrane surface. Based on the above, we propose a mechanism by which \*\*\*phospholamban\*\*\* regulates  $\text{Ca}^{2+}$  levels across membranes that takes into account both its selective ion conductance and \*\*\*inhibitory\*\*\* association with the  $\text{Ca}^{2+}$  pump.

=> d his

(FILE 'HOME' ENTERED AT 18:01:45 ON 11 AUG 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT 18:02:07 ON 11 AUG 2003

L1 5880 S PHOSPHOLAMBAN  
 L2 1548 S L1 (P) (INHIBIT? OR DEACTIVAT?)  
 L3 11269 S CYCLIC PEPTIDE  
 L4 0 S L2 (P) L3  
 L5 117423 S (MOLECULAR MODEL?) OR (COMPUTER MODEL?)  
 L6 15 S L2 (P) L5  
 L7 5 DUPLICATE REMOVE L6 (10 DUPLICATES REMOVED)

=> s cytosolic domain  
 L8 2126 CYTOSOLIC DOMAIN

=> s 18 (p) 11  
 L9 16 L8 (P) L1

=> s 19 (p) 12  
 L10 7 L9 (P) L2

=> duplicate remove 110

DUPLICATE PREFERENCE IS 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH'  
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n  
PROCESSING COMPLETED FOR L10  
L11 3 DUPLICATE REMOVE L10 (4 DUPLICATES REMOVED)

=> s l11 not l7  
L12 3 L11 NOT L7

=> d l12 1-3 ibib abs

L12 ANSWER 1 OF 3 MEDLINE on STN  
ACCESSION NUMBER: 91329371 MEDLINE  
DOCUMENT NUMBER: 91329371 PubMed ID: 1831047  
TITLE: Phospholamban is related to the autoinhibitory domain of the plasma membrane Ca(2+)-pumping ATPase.  
AUTHOR: Chiesi M; Vorherr T; Falchetto R; waelchli C; Carafoli E  
CORPORATE SOURCE: Department of Research, Pharmaceuticals Division, CIBA-GEIGY Limited, Basel, Switzerland.  
SOURCE: BIOCHEMISTRY, (1991 Aug 13) 30 (32) 7978-83.  
Journal code: 0370623. ISSN: 0006-2960.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199109  
ENTRY DATE: Entered STN: 19911006  
Last Updated on STN: 19970203  
Entered Medline: 19910913

AB The Ca<sup>2+</sup> pumps of the plasma membrane (PM ATPase) and of sarcoplasmic reticulum (SR ATPase) share a number of structural and functional properties. A major difference is the regulatory mechanism. The PM ATPase contains a C-terminal autoinhibitory domain; calmodulin binds to it, removing the \*\*\*inhibition\*\*\*. The SR ATPase contains a domain that interacts with the \*\*\*inhibitor\*\*\* protein \*\*\*phospholamban\*\*\* when the latter is in the nonphosphorylated state; phosphorylation of \*\*\*phospholamban\*\*\* removes the \*\*\*inhibition\*\*\*. Peptides corresponding to the autoinhibitory domain of the PM ATPase were synthesized and found to \*\*\*inhibit\*\*\* the SR ATPase. A 28-residue peptide (C28W), containing the entire autoinhibitory domain, was the most powerful (IC<sub>50</sub> = 15 microm; lmax greater than 90%). The \*\*\*inhibition\*\*\* was Ca<sup>2+</sup> dependent and more pronounced at submicromolar Ca<sup>2+</sup> concentrations. C28W is about 50% homologous to the \*\*\*cytosolic\*\*\* \*\*\*domain\*\*\* of \*\*\*phospholamban\*\*\*, the hydrophilic portion of which was found to interact directly with calmodulin (Kd = about 700 nM). However, while calmodulin reversed the \*\*\*inhibition\*\*\* of the SR ATPase by C28W, it failed to reverse that induced by nonphosphorylated \*\*\*phospholamban\*\*\*.

L12 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN  
ACCESSION NUMBER: 2003:235489 CAPLUS  
DOCUMENT NUMBER: 138:267695  
TITLE: \*\*\*Phospholamban\*\*\* \*\*\*cytosolic\*\*\*  
\*\*\*domain\*\*\* structure determined by NMR and its use in rational design of \*\*\*inhibitors\*\*\* of the ATPase activity of the enzyme  
INVENTOR(S): Pollesello, Piero; Ovaska, Martti; Tenhunen, Jukka; Vidgren, Jukka; Yliperttula-Ikonen, Marjo; Tilgmann, Carola; Lotta, Timo; Kaivola, Juha  
PATENT ASSIGNEE(S): Orion Corporation, Finland  
SOURCE: U.S., 58 pp., Cont.-in-part of U.S. Ser. No. 937,117, abandoned.  
CODEN: USXXAM  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6538022	B1	20030325	US 1999-252063	19990218
PRIORITY APPLN. INFO.:		US 1997-937117	B2	19970924

OTHER SOURCE(S): MARPAT 138:267695

AB The three-dimensional structure of the \*\*\*cytosolic\*\*\* \*\*\*domain\*\*\* of \*\*\*phospholamban\*\*\* (PLB) including the ATPase active site detd. from high resoln. NMR data. The structural information can be used in the rational design of of \*\*\*phospholamban\*\*\* \*\*\*inhibitors\*\*\*. Criteria for design of ligands and the synthesis of candidate compds. are

reported. Several of these compds. relieved the \*\*\*phospholamban\*\*\*  
\*\*\*inhibition\*\*\* of cal<sup>m</sup> uptake by vesicles of the sar<sup>m</sup>plasmic  
reticulum of cardiac muscle.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS  
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 3 OF 3 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN

ACCESSION NUMBER: 91:455981 SCISEARCH

THE GENUINE ARTICLE: GA940

TITLE: PHOSPHOLAMBAN IS RELATED TO THE AUTOINHIBITORY DOMAIN OF  
THE PLASMA-MEMBRANE CA<sup>2+</sup>-PUMPING ATPASE

AUTHOR: CHIESI M; VORHERR T; FALCHETTO R; WAELECHLI C; CARAFOLI E  
(Reprint)

CORPORATE SOURCE: CIBA GEIGY AG, DEPT RES, DIV PHARMACEUT, CH-4002 BASEL,  
SWITZERLAND; SWISS FED INST TECHNOL, DEPT BIOCHEM, CH-8092  
ZURICH, SWITZERLAND

COUNTRY OF AUTHOR: SWITZERLAND

SOURCE: BIOCHEMISTRY, (1991) Vol. 30, No. 32, pp. 7978-7983.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE

LANGUAGE: ENGLISH

REFERENCE COUNT: 30

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB The Ca<sup>2+</sup> pumps of the plasma membrane (PM ATPase) and of sarcoplasmic  
reticulum (SR ATPase) share a number of structural and functional  
properties. A major difference is the regulatory mechanism. The PM ATPase  
contains a C-terminal autoinhibitory domain; calmodulin binds to it,  
removing the \*\*\*inhibition\*\*\*. The SR ATPase contains a domain that  
interacts with the \*\*\*inhibitor\*\*\* protein \*\*\*phospholamban\*\*\*  
when the latter is in the nonphosphorylated state; phosphorylation of  
\*\*\*phospholamban\*\*\* removes the \*\*\*inhibition\*\*\*. Peptides  
corresponding to the autoinhibitory domain of the PM ATPase were  
synthesized and found to \*\*\*inhibit\*\*\* the SR ATPase. A 28-residue  
peptide (C28W), containing the entire autoinhibitory domain, was the most  
powerful (IC<sub>50</sub> = 15- $\mu$ M; I(max) > 90%). The \*\*\*inhibition\*\*\* was Ca<sup>2+</sup>  
dependent and more pronounced at submicromolar Ca<sup>2+</sup> concentrations. C28W  
is about 50% homologous to the \*\*\*cytosolic\*\*\* \*\*\*domain\*\*\* of  
\*\*\*phospholamban\*\*\*, the hydrophilic portion of which was found to  
interact directly with calmodulin (K(d) = about 700 nM). However, while  
calmodulin reversed the \*\*\*inhibition\*\*\* of the SR ATPase by C28W, it  
failed to reverse that induced by nonphosphorylated \*\*\*phospholamban\*\*\*.

=> s miller allan/au

L13 5 MILLER ALLAN/AU

=> s treco douglas/au

L14 23 TRECO DOUGLAS/AU

=> s selden richard/au

L15 7 SELDEN RICHARD/AU

=> s (l13 or l14 or l15) and l1

L16 0 (L13 OR L14 OR L15) AND L1

=> d his

(FILE 'HOME' ENTERED AT 18:01:45 ON 11 AUG 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT  
18:02:07 ON 11 AUG 2003

L1 5880 S PHOSPHOLAMBAN  
L2 1548 S L1 (P) (INHIBIT? OR DEACTIVAT?)  
L3 11269 S CYCLIC PEPTIDE  
L4 0 S L2 (P) L3  
L5 117423 S (MOLECULAR MODEL?) OR (COMPUTER MODEL?)  
L6 15 S L2 (P) L5  
L7 5 DUPLICATE REMOVE L6 (10 DUPLICATES REMOVED)  
L8 2126 S CYTOSOLIC DOMAIN  
L9 16 S L8 (P) L1  
L10 7 S L9 (P) L2  
L11 3 DUPLICATE REMOVE L10 (4 DUPLICATES REMOVED)  
L12 3 S L11 NOT L7  
L13 5 S MILLER ALLAN/AU  
L14 23 S TRECO DOUGLAS/AU  
L15 7 S SELDEN RICHARD/AU



L16

O S (L13 OR L14 OR L15) AND L1

=> logy

LOGY IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.

For a list of commands available to you in the current file, enter

"HELP COMMANDS" at an arrow prompt (=>).

=> log y

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

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48.17

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

ENTRY

SESSION

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-1.95

STN INTERNATIONAL LOGOFF AT 18:10:51 ON 11 AUG 2003